SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANTS: Emerson, Suzanne U., Purcell, Robert H., Tsarev, Sergei. A., and Robinson, Robin A.

    (ii) TITLE OF INVENTION: Recombinant Proteins Of A Pakistani Strain Of Hepatitis E And Their Use In Diagnostic Methods And Vaccines

    (iii) NUMBER OF SEQUENCES: 111

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: MORGAN & FINNEGAN
        (B) STREET: 345 PARK AVENUE
        (C) CITY: NEW YORK
        (D) STATE: NEW YORK
        (E) COUNTRY: USA
        (F) ZIP: 10154

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: FLOPPY DISK
        (B) COMPUTER: IBM PC COMPATIBLE
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: WORDPERFECT 5.1

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: 08/840,316
        (B) FILING DATE: 11-APR-1997
        (C) CLASSIFICATION

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Richard W. Bork
        (B) REGISTRATION NUMBER: 36,459
        (C) REFERENCE/DOCKET NUMBER: 2026-4255

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (212) 758-4800
        (B) TELEFAX: (212) 751-6849

(2) INFORMATION FOR SEQ ID NO: 1

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1693 AMINO ACID RESIDUES
        (B) TYPE: AMINO ACID
        (C) STRANDNESS: UNKNOWN
        (D) TOPOLOGY: UNKNOWN
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Glu Ala His Gln Phe Ile Lys Ala Pro Gly Ile Thr Thr Ala
1               5                   10                  15

Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser Ala Leu Ala Asn
                20                  25                  30
```

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```
Ala Val Val Val Arg Pro Phe Leu Ser His Gln Gln Ile Glu Ile
            35            40                45

Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe Arg Pro Glu
            50            55                60

Val Phe Trp Asn His Pro Ile Gln Arg Val Ile His Asn Glu Leu
            65            70                75

Glu Leu Tyr Cys Arg Ala Arg Ser Gly Arg Cys Leu Glu Ile Gly
            80            85                90

Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Val His Arg
            95            100               105

Cys Phe Leu Arg Pro Ala Gly Arg Asp Val Gln Arg Trp Tyr Thr
            110           115               120

Ala Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu
            125           130               135

Arg Gly Leu Pro Ala Ala Asp Arg Thr Tyr Cys Phe Asp Gly Phe
            140           145               150

Ser Gly Cys Asn Phe Pro Ala Glu Thr Gly Ile Ala Leu Tyr Ser
            155           160               165

Leu His Asp Met Ser Pro Ser Asp Val Ala Glu Ala Met Phe Arg
            170           175               180

His Gly Met Thr Arg Leu Tyr Ala Ala Leu His Leu Pro Pro Glu
            185           190               195

Val Leu Leu Pro Pro Gly Thr Tyr Arg Thr Ala Ser Tyr Leu Leu
            200           205               210

Ile His Asp Gly Arg Arg Val Val Val Thr Tyr Glu Gly Asp Thr
            215           220               225

Ser Ala Gly Tyr Asn His Asp Val Ser Asn Leu Arg Ser Trp Ile
         230           235              240

Arg Thr Thr Lys Val Thr Gly Asp His Pro Leu Val Ile Glu Arg
            245           250               255

Val Arg Ala Ile Gly Cys His Phe Val Leu Leu Leu Thr Ala Ala
            260           265               270

Pro Glu Pro Ser Pro Met Pro Tyr Val Pro Tyr Pro Arg Ser Thr
            275           280               285

Glu Val Tyr Val Arg Ser Ile Phe Gly Pro Gly Gly Thr Pro Ser
            290           295               300

Leu Phe Pro Thr Ser Cys Ser Thr Lys Ser Thr Phe His Ala Val
            305           310               315

Pro Ala His Ile Trp Asp Arg Leu Met Leu Phe Gly Ala Thr Leu
            320           325               330

Asp Asp Gln Ala Phe Cys Cys Ser Arg Leu Met Thr Tyr Leu Arg
            335           340               345
```

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```
Gly Ile Ser Tyr Lys Val Thr Val Gly Thr Leu Val Ala Asn Glu
            350             355             360

Gly Trp Asn Ala Ser Glu Asp Ala Leu Thr Ala Val Ile Thr Ala
            365             370             375

Ala Tyr Leu Thr Ile Cys His Gln Arg Tyr Leu Arg Thr Gln Ala
            380             385             390

Ile Ser Lys Gly Met Arg Arg Leu Glu Arg Glu His Ala Gln Lys
            395             400             405

Phe Ile Thr Arg Leu Tyr Ser Trp Leu Phe Glu Lys Ser Gly Arg
            410             415             420

Asp Tyr Ile Pro Gly Arg Gln Leu Glu Phe Tyr Ala Gln Cys Arg
            425             430             435

Arg Trp Leu Ser Ala Gly Phe His Leu Asp Pro Arg Val Leu Val
            440             445             450

Phe Asp Glu Ser Ala Pro Cys His Cys Arg Thr Ala Ile Arg Lys
            455             460             465

Ala Val Ser Lys Phe Cys Cys Phe Met Lys Trp Leu Gly Gln Glu
            470             475             480

Cys Thr Cys Phe Leu Gln Pro Ala Glu Gly Val Val Gly Asp Gln
            485             490             495

Gly His Asp Asn Glu Ala Tyr Glu Gly Ser Asp Val Asp Pro Ala
            500             505             510

Glu Ser Ala Ile Ser Asp Ile Ser Gly Ser Tyr Val Val Pro Gly
            515             520             525

Thr Ala Leu Gln Pro Leu Tyr Gln Ala Leu Asp Leu Pro Ala Glu
            530             535             540

Ile Val Ala Arg Ala Gly Arg Leu Thr Ala Thr Val Lys Val Ser
            545             550             555

Gln Val Asp Gly Arg Ile Asp Cys Glu Thr Leu Leu Gly Asn Lys
            560             565             570

Thr Phe Arg Thr Ser Phe Val Asp Gly Ala Val Leu Glu Thr Asn
            575             580             585

Gly Pro Glu Arg His Asn Leu Ser Phe Asp Ala Ser Gln Ser Thr
            590             595             600

Met Ala Ala Gly Pro Phe Ser Leu Thr Tyr Ala Ala Ser Ala Ala
            605             610             615

Gly Leu Glu Val Arg Tyr Val Ala Ala Gly Leu Asp His Arg Ala
            620             625             630

Val Phe Ala Pro Gly Val Ser Pro Arg Ser Ala Pro Gly Glu Val
            635             640             645

Thr Ala Phe Cys Ser Ala Leu Tyr Arg Phe Asn Arg Glu Ala Gln
            650             655             660
```

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Arg Leu Ser Leu Thr Gly Asn Phe Trp Phe His Pro Glu Gly Leu
            665   670   675

Leu Gly Pro Phe Ala Pro Phe Ser Pro Gly His Val Trp Glu Ser
            680   685   690

Ala Asn Pro Phe Cys Gly Glu Ser Thr Leu Tyr Thr Arg Thr Trp
            695   700   705

Ser Glu Val Asp Ala Val Pro Ser Pro Ala Gln Pro Asp Leu Gly
            710   715   720

Phe Thr Ser Glu Pro Ser Ile Pro Ser Arg Ala Ala Thr Pro Thr
            725   730   735

Pro Ala Ala Pro Leu Pro Pro Pro Ala Pro Asp Pro Ser Pro Thr
            740   745   750

Leu Ser Ala Pro Ala Arg Gly Glu Pro Ala Pro Gly Ala Thr Ala
            755   760   765
Arg Ala Pro Ala Ile Thr His Gln Thr Ala Arg His Arg Arg Leu
            770   775   780

Leu Phe Thr Tyr Pro Asp Gly Ser Lys Val Phe Ala Gly Ser Leu
            785   790   795

Phe Glu Ser Thr Cys Thr Trp Leu Val Asn Ala Ser Asn Val Asp
            800   805   810

His Arg Pro Gly Gly Gly Leu Cys His Ala Phe Tyr Gln Arg Tyr
            815   820   825

Pro Ala Ser Phe Asp Ala Ala Ser Phe Val Met Arg Asp Gly Ala
            830   835   840

Ala Ala Tyr Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala
            845   850   855

Pro Asp Tyr Arg Leu Glu His Asn Pro Lys Arg Leu Glu Ala Ala
            860   865   870

Tyr Arg Glu Thr Cys Ser Arg Leu Gly Thr Ala Ala Tyr Pro Leu
            875   880   885

Leu Gly Thr Gly Ile Tyr Gln Val Pro Ile Gly Pro Ser Phe Asp
            890   895   900

Ala Trp Glu Arg Asn His Arg Pro Gly Asp Glu Leu Tyr Leu Pro
            905   910   915

Glu Leu Ala Ala Arg Trp Phe Glu Ala Asn Arg Pro Thr Cys Pro
            920   925   930

Thr Leu Thr Ile Thr Glu Asp Val Ala Arg Thr Ala Asn Leu Ala
            935   940   945

Ile Glu Leu Asp Ser Ala Thr Asp Val Gly Arg Ala Cys Ala Gly
            950   955   960

Cys Arg Val Thr Pro Gly Val Val Gln Tyr Gln Phe Thr Ala Gly
            965   970   975

Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Thr Gln Ala Asp Val
            980   985   990

```
Asp Val Val Val Val Pro Thr Arg Glu Leu Arg Asn Ala Trp Arg
              995               1000               1005

Arg Arg Gly Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg Val
              1010              1015               1020

Thr Gln Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro
              1025              1030               1035

Pro His Leu Leu Leu Leu His Met Gln Arg Ala Ala Thr Val His
              1040              1045               1050

Leu Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His
              1055              1060               1065

Ala Gly Leu Val Pro Ala Ile Arg Pro Asp Leu Ala Pro Thr Ser
              1070              1075               1080

Trp Trp His Val Thr His Arg Cys Pro Ala Asp Val Cys Glu Leu
              1085              1090               1095

Ile Arg Gly Ala Tyr Pro Met Ile Gln Thr Thr Ser Arg Val Leu
              1100              1105               1110

Arg Ser Leu Phe Trp Gly Glu Pro Ala Val Gly Gln Lys Leu Val
              1115              1120               1125

Phe Thr Gln Ala Ala Lys Ala Ala Asn Pro Gly Ser Val Thr Val
              1130              1135               1140

His Glu Ala Gln Gly Ala Thr Tyr Thr Glu Thr Thr Ile Ile Ala
              1145              1150               1155

Thr Ala Asp Ala Arg Gly Leu Ile Gln Ser Ser Arg Ala His Ala
         1160         1165              1170

Ile Val Ala Leu Thr Arg His Thr Glu Lys Cys Val Ile Ile Asp
              1175              1180               1185

Ala Pro Gly Leu Leu Arg Glu Val Gly Ile Ser Asp Ala Ile Val
              1190              1195               1200

Asn Asn Phe Phe Leu Ala Gly Gly Glu Ile Gly His Gln Arg Pro
              1205              1210               1215

Ser Val Ile Pro Arg Gly Asn Pro Asp Ala Asn Val Asp Thr Leu
              1220              1225               1230

Ala Ala Phe Pro Pro Ser Cys Glu Ile Ser Ala Phe His Glu Leu
              1235              1240               1245

Ala Glu Glu Leu Gly His Arg Pro Ala Pro Val Ala Ala Val Leu
              1250              1255               1260

Pro Pro Cys Pro Glu Leu Glu Gln Gly Leu Leu Tyr Leu Pro Gln
              1265              1270               1275

Glu Leu Thr Thr Cys Asp Ser Val Val Thr Phe Glu Leu Thr Asp
              1280              1285               1290
```

315661_1

```
Ile Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val
            1295              1300              1305

Leu Ser Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr
            1310              1315              1320

Asn Ala Ser His Ser Asp Val Arg Asp Ser Leu Ala Arg Phe Ile
            1325              1330              1335

Pro Ala Ile Gly Pro Val Gln Val Thr Thr Cys Glu Leu Tyr Glu
            1340              1345              1350

Leu Glu Glu Ala Met Val Glu Lys Gly Gln Asp Gly Ser Ala Val
            1355              1360              1365

Leu Glu Leu Asp Leu Cys Ser Arg Asp Val Ser Arg Ile Thr Phe
            1370              1375              1380

Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr Ile Ala
            1385              1390              1395

His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe
            1400              1405              1410

Cys Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Ala Ile
            1415              1420              1425

Leu Ala Leu Leu Pro Gln Gly Val Phe Tyr Gly Asp Ala Phe Asp
            1430              1435              1440

Asp Thr Val Phe Ser Ala Ala Val Ala Ala Ala Lys Ala Ser Met
            1445              1450              1455

Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn
            1460              1465              1470

Phe Ser Leu Gly Leu Glu Cys Ala Ile Met Glu Glu Cys Gly Met
            1475              1480              1485

Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Ile Arg Ser Ala Trp
            1490              1495              1500

Ile Leu Gln Ala Pro Lys Glu Ser Leu Arg Gly Phe Trp Lys Lys
            1505              1510              1515

His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn
            1520              1525              1530

Met Ala Val Ile Thr His Cys Tyr Asp Phe Arg Asp Leu Gln Val
            1535              1540              1545

Ala Ala Phe Lys Gly Asp Asp Ser Ile Val Leu Cys Ser Glu Tyr
            1550              1555              1560

Arg Gln Ser Pro Gly Ala Ala Val Leu Ile Ala Gly Cys Gly Leu
            1565              1570              1575

Lys Leu Lys Val Asp Phe Arg Pro Ile Gly Leu Tyr Ala Gly Val
            1580              1585              1590

Val Val Ala Pro Gly Leu Gly Ala Leu Pro Asp Val Val Arg Phe
            1595              1600              1605
```

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```
Ala Gly Arg Leu Thr Glu Lys Asn Trp Gly Pro Gly Pro Glu Arg
              1610              1615              1620

Ala Glu Gln Leu Arg Leu Ala Val Ser Asp Phe Leu Arg Lys Leu
          1625              1630              1635

Thr Asn Val Ala Gln Met Cys Val Asp Val Val Ser Arg Val Tyr
              1640              1645              1650

Gly Val Ser Pro Gly Leu Val His Asn Leu Ile Glu Met Leu Gln
              1655              1660              1665

Ala Val Ala Asp Gly Lys Ala His Phe Thr Glu Ser Val Lys Pro
              1670              1675              1680

Val Leu Asp Leu Thr Asn Ser Ile Leu Cys Arg Val Glu
              1685              1690
```

(2)   INFORMATION FOR SEQ ID NO: 2:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 660 amino acid residues
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: unknown
        (D)   TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Arg Pro Arg Pro Ile Leu Leu Leu Leu Leu Met Phe Leu Pro
1             5                  10                 15

Met Leu Pro Ala Pro Pro Gly Gln Pro Ser Gly Arg Arg Arg
              20             25                 30

Gly Arg Arg Ser Gly Gly Ser Gly Gly Gly Phe Trp Gly Asp Arg
              35             40                 45

Val Asp Ser Gln Pro Phe Ala Ile Pro Tyr Ile His Pro Thr Asn
              50             55                 60

Pro Phe Ala Pro Asp Val Thr Ala Ala Ala Gly Ala Gly Pro Arg
              65             70                 75

Val Arg Gln Pro Ala Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln
              80             85                 90

Ala Gln Arg Pro Ala Ala Ala Ser Arg Arg Arg Pro Thr Thr Ala
              95             100                105

Gly Ala Ala Pro Leu Thr Ala Val Ala Pro Ala His Asp Thr Pro
              110            115                120

Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
              125            130                135

Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala Thr Gly
              140            145                150

Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Ser Pro Leu Leu Pro
              155            160                165

Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser
              170            175                180
```

```
Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile Arg Tyr Arg
                185                     190                 195

Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser
                200                     205                 210

Phe Tyr Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met Asn
                215                     220                 225

Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile
                230                     235                 240

Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn
                245                     250                 255

Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu
                260                     265                 270

Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val
                275                     280                 285

Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu
                290                     295                 300

Asp Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn
                305                     310                 315

Thr Asn Thr Arg Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg
                320                     325                 330

Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala
                335                     340                 345

Ala Thr Arg Phe Met Lys Asp Leu Tyr Phe Thr Ser Thr Asn Gly
                350                     355                 360

Val Gly Glu Ile Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu
                365                     370                 375

Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser
                380                     385                 390

Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn
                395                     400                 405

Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln
                410                     415                 420

Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp Leu Gly Glu
                425                     430                 435

Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp
                440                     445                 450

Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu
                455                     460                 465

Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr
                470                     475                 480

Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val Ser
                485                     490                 495
```

315661_1

```
Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val
            500                 505                     510

Ala Arg Ser Leu Asp Trp Thr Lys Val Thr Leu Asp Gly Arg Pro
            515                 520                     525

Leu Ser Thr Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro
            530                 535                     540

Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala
            545                 550                     555

Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu
            560                 565                     570

Val Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr
            575                 580                     585

Thr Ser Leu Gly Ala Gly Pro Val Ser Ile Ser Ala Val Ala Val
            590                 595                     600

Leu Ala Pro His Ser Val Leu Ala Leu Leu Glu Asp Thr Met Asp
            605                 610                     615

Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys
            620                 625                     630

Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val Ala
            635                 640                     645

Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Leu
            650                 655                     660
```

(2)   INFORMATION FOR SEQ ID NO: 3:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 123 amino acid residues
       (B)   TYPE: amino acid
       (C)   STRANDEDNESS: unknown
       (D)   TOPOLOGY: unknown

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Asn Asn Met Ser Phe Ala Ala Pro Met Gly Ser Arg Pro Cys
1               5                   10                      15

Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys
                20                  25                      30

Cys Pro Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly
                35                  40                      45

Gly Ala Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu
                50                  55                      60

Ile Leu Ser Pro Ser Gln Ser Pro Ile Phe Ile Gln Pro Thr Pro
                65                  70                      75

Ser Pro Pro Met Ser Pro Leu Arg Pro Gly Leu Asp Leu Val Phe
                80                  85                      90
```

Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro
              95   100   105

Ser Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly
              110   115   120

Pro Arg Arg

(2)   INFORMATION FOR SEQ ID NO: 4:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 7168 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGCAGACCA CATATGTGGT CGATGCCATG GAGGCCCATC AGTTTATCAA   50

GGCTCCTGGC ATCACTACTG CTATTGAGCA GGCTGCTCTA GCAGCGGCCA   100

ACTCTGCCCT TGCGAATGCT GTGGTAGTTA GGCCTTTTCT CTCTCACCAG   150

CAGATTGAGA TCCTTATTAA CCTAATGCAA CCTCGCCAGC TTGTTTTCCG   200

CCCCGAGGTT TTCTGGAACC ATCCCATCCA GCGTGTTATC CATAATGAGC   250

TGGAGCTTTA CTGTCGCGCC CGCTCCGGCC GCTGCCTCGA AATTGGTGCC   300

CACCCCCGCT CAATAAATGA CAATCCTAAT GTGGTCCACC GTTGCTTCCT   350

CCGTCCTGCC GGGCGTGATG TTCAGCGTTG GTATACTGCC CCTACCCGCG   400

GGCCGGCTGC TAATTGCCGG CGTTCCGCGC TGCGCGGGCT CCCCGCTGCT   450

GACCGCACTT ACTGCTTCGA CGGGTTTTCT GGCTGTAACT TTCCCGCCGA   500

GACGGGCATC GCCCTCTATT CTCTCCATGA TATGTCACCA TCTGATGTCG   550

CCGAGGCTAT GTTCCGCCAT GGTATGACGC GGCTTTACGC TGCCCTCCAC   600

CTCCCGCCTG AGGTCCTGTT GCCCCCTGGC ACATACCGCA CCGCGTCGTA   650

CTTGCTGATC CATGACGGCA GGCGCGTTGT GGTGACGTAT GAGGGTGACA   700

CTAGTGCTGG TTATAACCAC GATGTTTCCA ACCTGCGCTC CTGGATTAGA   750

ACCACTAAGG TTACCGGAGA CCACCCTCTC GTCATCGAGC GGGTTAGGGC   800

CATTGGCTGC CACTTTGTCC TTTTACTCAC GGCTGCTCCG GAGCCATCAC   850

CTATGCCCTA TGTCCCTTAC CCCCGGTCTA CCGAGGTCTA TGTCCGATCG   900

ATCTTCGGCC CGGGTGGCAC CCCCTCCCTA TTTCCAACCT CATGCTCCAC   950

CAAGTCGACC TTCCATGCTG TCCCTGCCCA TATCTGGGAC CGTCTCATGT   1000

TGTTCGGGGC CACCCTAGAT GACCAAGCCT TTTGCTGCTC CCGCCTAATG   1050

ACTTACCTCC GCGGCATTAG CTACAAGGTT ACTGTGGGCA CCCTTGTTGC   1100

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```
CAATGAAGGC TGGAACGCCT CTGAGGACGC TCTTACAGCT GTCATCACTG   1150

CCGCCTACCT TACCATCTGC CACCAGCGGT ACCTCCGCAC TCAGGCTATA   1200

TCTAAGGGGA TGCGTCGCCT GGAGCGGGAG CATGCTCAGA AGTTTATAAC   1250

ACGCCTCTAC AGTTGGCTCT TTGAGAAGTC CGGCCGTGAT TATATCCCCG   1300

GCCGTCAGTT GGAGTTCTAC GCTCAGTGTA GGCGCTGGCT CTCGGCCGGC   1350

TTTCATCTTG ACCCACGGGT GTTGGTTTTT GATGAGTCGG CCCCCTGCCA   1400

CTGTAGGACT GCGATTCGTA AGGCGGTCTC AAAGTTTTGC TGCTTTATGA   1450

AGTGGCTGGG CCAGGAGTGC ACCTGTTTTC TACAACCTGC AGAAGGCGTC   1500

GTTGGCGACC AGGGCCATGA CAACGAGGCC TATGAGGGGT CTGATGTTGA   1550

CCCTGCTGAA TCCGCTATTA GTGACATATC TGGGTCCTAC GTAGTCCCTG   1600

GCACTGCCCT CCAACCGCTT TACCAAGCCC TTGACCTCCC CGCTGAGATT   1650

GTGGCTCGTG CAGGCCGGCT GACCGCCACA GTAAAGGTCT CCCAGGTCGA   1700

CGGGCGGATC GATTGTGAGA CCCTTCTCGG TAATAAAACC TTCCGCACGT   1750

CGTTTGTTGA CGGGGCGGTT TTAGAGACTA ATGGCCCAGA GCGCCACAAT   1800

CTCTCTTTTG ATGCCAGTCA GAGCACTATG GCCGCCGGCC CTTTCAGTCT   1850

CACCTATGCC GCCTCTGCTG CTGGGCTGGA GGTGCGCTAT GTCGCCGCCG   1900

GGCTTGACCA CCGGGCGGTT TTTGCCCCCG GCGTTTCACC CCGGTCAGCC   1950

CCTGGCGAGG TCACCGCCTT CTGTTCTGCC CTATACAGGT TTAATCGCGA   2000

GGCCCAGCGC CTTTCGCTGA CCGGTAATTT TTGGTTCCAT CCTGAGGGGC   2050

TCCTTGGCCC CTTTGCCCCG TTTTCCCCCG GGCATGTTTG GGAGTCGGCT   2100

AATCCATTCT GTGGCGAGAG CACACTTTAC ACCCGCACTT GGTCGGAGGT   2150

TGATGCTGTT CCTAGTCCAG CCCAGCCCGA CTTAGGTTTT ACATCTGAGC   2200

CTTCTATACC TAGTAGGGCC GCCACACCTA CCCCGGCGGC CCCTCTACCC   2250

CCCCCTGCAC CGGATCCTTC CCCTACTCTC TCTGCTCCGG CGCGTGGTGA   2300

GCCGGCTCCT GGCGCTACCG CCAGGGCCCC AGCCATAACC CACCAGACGG   2350

CCCGGCATCG CCGCCTGCTC TTTACCTACC CGGATGGCTC TAAGGTGTTC   2400

GCCGGCTCGC TGTTTGAGTC GACATGTACC TGGCTCGTTA ACGCGTCTAA   2450

TGTTGACCAC CGCCCTGGCG GTGGGCTCTG TCATGCATTT TACCAGAGGT   2500

ACCCCGCCTC CTTTGATGCT GCCTCTTTTG TGATGCGCGA CGGCGCGGCC   2550

GCCTACACAT TAACCCCCCG GCCAATAATT CATGCCGTCG CTCCTGATTA   2600

TAGGTTGGAA CATAACCCAA AGAGGCTTGA GGCTGCCTAC CGGGAGACTT   2650

GCTCCCGCCT CGGTACCGCT GCATACCCAC TCCTCGGGAC CGGCATATAC   2700
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315661_1

```
CAGGTGCCGA TCGGTCCCAG TTTTGACGCC TGGGAGCGGA ATCACCGCCC 2750

CGGGGACGAG TTGTACCTTC CTGAGCTTGC TGCCAGATGG TTCGAGGCCA 2800

ATAGGCCGAC CTGCCCAACT CTCACTATAA CTGAGGATGT TGCGCGGACA 2850

GCAAATCTGG CTATCGAACT TGACTCAGCC ACAGACGTCG GCCGGGCCTG 2900

TGCCGGCTGT CGAGTCACCC CCGGCGTTGT GCAGTACCAG TTTACCGCAG 2950

GTGTGCCTGG ATCCGGCAAG TCCCGCTCTA TTACCCAAGC CGACGTGGAC 3000

GTTGTCGTGG TCCCGACCCG GGAGTTGCGT AATGCCTGGC GCCGCCGCGG 3050

CTTCGCTGCT TTCACCCCGC ACACTGCGGC TAGAGTCACC CAGGGGCGCC 3100

GGGTTGTCAT TGATGAGGCC CCGTCCCTTC CCCCTCATTT GCTGCTGCTC 3150

CACATGCAGC GGGCCGCCAC CGTCCACCTT CTTGGCGACC CGAATCAGAT 3200

CCCAGCCATC GATTTTGAGC ACGCCGGGCT CGTTCCCGCC ATCAGGCCCG 3250

ATTTGGCCCC CACCTCCTGG TGGCATGTTA CCCATCGCTG CCCTGCGGAT 3300

GTATGTGAGC TAATCCGCGG CGCATACCCT ATGATTCAGA CCACTAGTCG 3350

GGTCCTCCGG TCGTTGTTCT GGGGTGAGCC CGCCGTTGGG CAGAAGCTAG 3400

TGTTCACCCA GGCGGCTAAG GCCGCCAACC CCGGTTCAGT GACGGTCCAT 3450

GAGGCACAGG GCGCTACCTA CACAGAGACT ACCATCATTG CCACGGCAGA 3500

TGCTCGAGGC CTCATTCAGT CGTCCCGAGC TCATGCCATT GTTGCCTTGA 3550

CGCGCCACAC TGAGAAGTGC GTCATCATTG ACGCACCAGG CCTGCTTCGC 3600

GAGGTGGGCA TCTCCGATGC AATCGTTAAT AACTTTTTCC TTGCTGGTGG 3650

CGAAATTGGC CACCAGCGCC CATCTGTTAT CCCTCGCGGC AATCCTGACG 3700

CCAATGTTGA CACCTTGGCT GCCTTCCCGC CGTCTTGCCA GATTAGCGCC 3750

TTCCATCAGT TGGCTGAGGA GCTTGGCCAC AGACCTGCCC CTGTCGCGGC 3800

TGTTCTACCG CCCTGCCCTG AGCTTGAACA GGGCCTTCTC TACCTGCCCC 3850

AAGAACTCAC CACCTGTGAT AGTGTCGTAA CATTTGAATT AACAGATATT 3900

GTGCATTGTC GTATGGCCGC CCCGAGCCAG CGCAAGGCCG TGCTGTCCAC 3950

GCTCGTGGGC CGTTATGGCC GCCGCACAAA GCTCTACAAT GCCTCCCACT 4000

CTGATGTTCG CGACTCTCTC GCCCGTTTTA TCCCGGCCAT TGGCCCCGTA 4050

CAGGTTACAA CCTGTGAATT GTACGAGCTA GTGGAGGCCA TGGTCGAGAA 4100

GGGCCAGGAC GGCTCCGCCG TCCTTGAGCT CGACCTTTGT AGCCGCGACG 4150

TGTCCAGGAT CACCTTCTTC CAGAAAGATT GTAATAAATT CACCACGGGG 4200

GAGACCATCG CCCATGGTAA AGTGGGCCAG GGCATTTCGG CCTGGAGTAA 4250
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GACCTTCTGT GCCCTTTTCG GCCCCTGGTT CCGTGCTATT GAGAAGGCTA    4300

TCCTGGCCCT GCTCCCTCAG GGTGTGTTTT ATGGGGATGC CTTTGATGAC    4350

ACCGTCTTCT CGGCGGCTGT GGCCGCAGCA AAGGCATCCA TGGTGTTCGA    4400

GAATGACTTT TCTGAGTTTG ATTCCACCCA GAATAATTTT TCCTTGGGCC    4450

TAGAGTGTGC TATTATGGAG GAGTGTGGGA TGCCGCAGTG GCTCATCCGC    4500

TTGTACCACC TTATAAGGTC TGCGTGGATT CTGCAGGCCC CGAAGGAGTC    4550

CCTGCGAGGG TTTTGGAAGA AACACTCCGG TGAGCCCGGC ACCCTTCTGT    4600

GGAATACTGT CTGGAACATG GCCGTTATCA CCCACTGTTA TGATTTCCGC    4650

GATCTGCAGG TGGCTGCCTT TAAAGGTGAT GATTCGATAG TGCTTTGCAG    4700

TGAGTACCGT CAGAGCCCAG GGGCTGCTGT CCTGATTGCT GGCTGTGGCC    4750

TAAAGTTGAA GGTGGATTTC CGTCCGATTG GTCTGTATGC AGGTGTTGTG    4800

GTGGCCCCCG GCCTTGGCGC GCTTCCTGAT GTCGTGCGCT TCGCCGGTCG    4850

GCTTACTGAG AAGAATTGGG GCCCTGGCCC CGAGCGGGCG GAGCAGCTCC    4900

GCCTCGCTGT GAGTGATTTT CTCCGCAAGC TCACGAATGT AGCTCAGATG    4950

TGTGTGGATG TTGTCTCTCG TGTTTATGGG GTTTCCCCTG GGCTCGTTCA    5000

TAACCTGATT GGCATGCTAC AGGCTGTTGC TGATGGCAAG GCTCATTTCA    5050

CTGAGTCAGT GAAGCCAGTG CTTGACCTGA CAAATTCAAT TCTGTGTCGG    5100

GTGGAATGAA TAACATGTCT TTTGCTGCGC CCATGGGTTC GCGACCATGC    5150

GCCCTCGGCC TATTTTGCTG TTGCTCCTCA TGTTTCTGCC TATGCTGCCC    5200

GCGCCACCGC CCGGTCAGCC GTCTGGCCGC CGTCGTGGGC GGCGCAGCGG    5250

CGGTTCCGGC GGTGGTTTCT GGGGTGACCG GGTTGATTCT CAGCCCTTCG    5300

CAATCCCCTA TATTCATCCA ACCAACCCCT TCGCCCCCGA TGTCACCGCT    5350

GCGGCCGGGG CTGGACCTCG TGTTCGCCAA CCCGCCCGAC CACTCGGCTC    5400

CGCTTGGCGT GACCAGGCCC AGCGCCCGC CGCTGCCTCA CGTCGTAGAC    5450

CTACCACAGC TGGGGCCGCG CCGCTAACCG CGGTCGCTCC GGCCCATGAC    5500

ACCCCGCCAG TGCCTGATGT TGACTCCCGC GGCGCCATCC TGCGCCGGCA    5550

GTATAACCTA TCAACATCTC CCCTCACCTC TTCCGTGGCC ACCGGCACAA    5600

ATTTGGTTCT TTACGCCGCT CCTCTTAGCC CGCTTCTACC CCTCCAGGAC    5650

GGCACCAATA CTCATATAAT GGCTACAGAA GCTTCTAATT ATGCCAGTA    5700

CCGGGTTGCT CGTGCCACAA TTCGCTACCG CCCGCTGGTC CCCAACGCTG    5750

TTGGTGGCTA CGCTATCTCC ATTTCGTTCT GGCCACAGAC CACCACCACC    5800

CCGACGTCCG TTGACATGAA TTCAATAACC TCGACGGATG TCCGTATTTT    5850
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AGTCCAGCCC GGCATAGCCT CCGAGCTTGT TATTCCAAGT GAGCGCCTAC    5900

ACTATCGCAA CCAAGGTTGG CGCTCTGTTG AGACCTCCGG GGTGGCGGAG    5950

GAGGAGGCCA CCTCTGGTCT TGTCATGCTC TGCATACATG GCTCACCTGT    6000

AAATTCTTAT ACTAATACAC CCTATACCGG TGCCCTCGGG CTGTTGGACT    6050

TTGCCCTCGA ACTTGAGTTC CGCAACCTCA CCCCCGGTAA TACCAATACG    6100

CGGGTCTCGC GTTACTCCAG CACTGCCCGT CACCGCCTTC GTCGCGGTGC    6150

AGATGGGACT GCCGAGCTCA CCACCACGGC TGCTACTCGC TTCATGAAGG    6200

ACCTCTATTT TACTAGTACT AATGGTGTTG GTGAGATCGG CCGCGGGATA    6250

GCGCTTACCC TGTTTAACCT TGCTGACACC CTGCTTGGCG GTCTACCGAC    6300

AGAATTGATT TCGTCGGCTG GTGGCCAGCT GTTCTACTCT CGCCCCGTCG    6350

TCTCAGCCAA TGGCGAGCCG ACTGTTAAGC TGTATACATC TGTGGAGAAT    6400

GCTCAGCAGG ATAAGGGTAT TGCAATCCCG CATGACATCG ACCTCGGGGA    6450

ATCCCGTGTA GTTATTCAGG ATTATGACAA CCAACATGAG CAGGACCGAC    6500

CGACACCTTC CCCAGCCCCA TCGCGTCCTT TTTCTGTCCT CCGAGCTAAC    6550

GATGTGCTTT GGCTTTCTCT CACCGCTGCC GAGTATGACC AGTCCACTTA    6600

CGGCTCTTCG ACCGGCCCAG TCTATGTCTC TGACTCTGTG ACCTTGGTTA    6650

ATGTTGCGAC CGGCGCGCAG GCCGTTGCCC GGTCACTCGA CTGGACCAAG    6700

GTCACACTTG ATGGTCGCCC CCTTTCCACC ATCCAGCAGT ATTCAAAGAC    6750

CTTCTTTGTC CTGCCGCTCC GCGGTAAGCT CTCCTTTTGG GAGGCAGGAA    6800

CTACTAAAGC CGGGTACCCT TATAATTATA ACACCACTGC TAGTGACCAA    6850

CTGCTCGTTG AGAATGCCGC TGGGCATCGG GTTGCTATTT CCACCTACAC    6900

TACTAGCCTG GGTGCTGGCC CCGTCTCTAT TTCCGCGGTT GCTGTTTTAG    6950

CCCCCCACTC TGTGCTAGCA TTGCTTGAGG ATACCATGGA CTACCCTGCC    7000

CGCGCCCATA CTTTCGATGA CTTCTGCCCG GAGTGCCGCC CCCTTGGCCT    7050

CCAGGGTTGT GCTTTTCAGT CTACTGTCGC TGAGCTTCAG CGCCTTAAGA    7100

TGAAGGTGGG TAAAACTCGG GAGTTATAGT TTATTTGCTT GTGCCCCCCT    7150

TCTTTCTGTT GCTTATTT                                      7168
```

(2)   INFORMATION FOR SEQ ID NO: 5:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 25 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

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(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACATTTGAAT TCACAGACAT TGTGC   25

(2)   INFORMATION FOR SEQ ID NO: 6:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 26 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACACAGATCT GAGCTACATT CGTGAG   26

(2)   INFORMATION FOR SEQ ID NO: 7:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 26 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGGGATCC ATGGTGTTTG AGAATG   26

(2)   INFORMATION FOR SEQ ID NO: 8:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 25 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTCACTGCA GAGCACTATC GAATC   25

(2)   INFORMATION FOR SEQ ID NO: 9:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 22 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGTAAACTG GTACTGCACA AC   22

(2)   INFORMATION FOR SEQ ID NO: 10:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 22 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAGTCCCGCT CTATTACCCA AG   22

(2)   INFORMATION FOR SEQ ID NO: 11:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCCACGGGT GTTGGTTTTT G   21

(2)   INFORMATION FOR SEQ ID NO: 12:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCTTGGGGC AGGTAGAGAA G   21

(2)   INFORMATION FOR SEQ ID NO: 13:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 26 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTATTGAATT CATGTCAACG GACGTC   26

(2)   INFORMATION FOR SEQ ID NO: 14:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATAATTCAT GCCGTCGCTC C   21

(2)   INFORMATION FOR SEQ ID NO: 15:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 21 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTCAGGA AGGTACAACT C   21

(2)   INFORMATION FOR SEQ ID NO: 16:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 24 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATCGATGG CTGGGATCTG ATTC   24

(2)   INFORMATION FOR SEQ ID NO: 17:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 21 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGGCATTGT AGAGCTTTGT G   21

(2)   INFORMATION FOR SEQ ID NO: 18:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 22 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGTTGCAC GGACAGCAAA TC   22

(2)   INFORMATION FOR SEQ ID NO: 19:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 24 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCTCCGATG CAATCGTTAA TAAC   24

(2)   INFORMATION FOR SEQ ID NO: 20:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 21 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAATCCATTC TGTGGCGAGA G   21

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(2) INFORMATION FOR SEQ ID NO: 21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGTGTGACC TTGGTCCAGT C   21

(2) INFORMATION FOR SEQ ID NO: 22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGCTCGTGC CACAATTCGC TAC   23

(2) INFORMATION FOR SEQ ID NO: 23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTTCACTG AGTCAGTGAA G   21

(2) INFORMATION FOR SEQ ID NO: 24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TAATTATAAC ACCACTGCTA G   21

(2) INFORMATION FOR SEQ ID NO: 25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATTGCAATA CCCTTATCCT G   21

(2) INFORMATION FOR SEQ ID NO: 26:

    (i) SEQUENCE CHARACTERISTICS:

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                    (A)   LENGTH: 23 base pairs
                    (B)   TYPE:  nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY:  linear

           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:26:

           ATTAAACCTG TATAGGGCAG AAC                          23

    (2)   INFORMATION FOR SEQ ID NO: 27:

           (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 21 base pairs
                    (B)   TYPE:  nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY:  linear


           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:27:

           AAGTTCGATA GCCAGATTTG C                            21

    (2)   INFORMATION FOR SEQ ID NO: 28:

           (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 21 base pairs
                    (B)   TYPE:  nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY:  linear


           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:28:

           TCATGTTGGT TGTCATAATC C                            21

    (2)   INFORMATION FOR SEQ ID NO: 29:

           (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 21 base pairs
                    (B)   TYPE:  nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY:  linear

           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:29:

           GATGACGCAC TTCTCAGTGT G                            21

    (2)   INFORMATION FOR SEQ ID NO: 30:

           (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 19 base pairs
                    (B)   TYPE:  nucleic acid
                    (C)   STRANDEDNESS: single
                    (D)   TOPOLOGY:  linear

           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:30:

           AGAACAACGA ACGGAGAAC                               19

    (2)   INFORMATION FOR SEQ ID NO: 31:

           (i)   SEQUENCE CHARACTERISTICS:
                    (A)   LENGTH: 21 base pairs
                    (B)   TYPE:  nucleic acid
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```
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY:  linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:31:

    AGATCCCAGC CATCGACTTT G                                    21


(2)  INFORMATION FOR SEQ ID NO: 32:

    (i)    SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE:  nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY:  linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:32:

    TAGTAGTGTA GGTGGAAATA G                                    21

(2)  INFORMATION FOR SEQ ID NO: 33:

    (i)    SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE:  nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY:  linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:33:

    GTGTGGTTAT TCAGGATTAT G                                    21

(2)  INFORMATION FOR SEQ ID NO: 34:

    (i)    SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE:  nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY:  linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:34:

    ACTCTGTGAC CTTGGTTAAT G                                    21

(2)  INFORMATION FOR SEQ ID NO: 35:

    (i)    SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE:  nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY:  linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:35:

    AACTCAAGTT CGAGGGCAAA G                                    21

(2)  INFORMATION FOR SEQ ID NO: 36:

    (i)    SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE:  nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGCTTACCCT GTTTAACCTT G   21

(2)   INFORMATION FOR SEQ ID NO: 37:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 24 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCCCCTATA TTCATCCAAC CAAC   24

(2)   INFORMATION FOR SEQ ID NO: 38:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTCCTCATGT TTCTGCCTAT G   21

 (2)   INFORMATION FOR SEQ ID NO: 39:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 22 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCCAGAACGA AATGGAGATA GC   22

(2)   INFORMATION FOR SEQ ID NO: 40:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCAGACATA AAACCTAAGT C   21

(2)   INFORMATION FOR SEQ ID NO: 41:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)   LENGTH: 21 base pairs
          (B)   TYPE: nucleic acid
          (C)   STRANDEDNESS: single
          (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:41:

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TGCCCTATAC AGGTTTAATC G   21

(2)   INFORMATION FOR SEQ ID NO: 42:

   (i)   SEQUENCE CHARACTERISTICS:
     (A)   LENGTH: 19 base pairs
     (B)   TYPE: nucleic acid
     (C)   STRANDEDNESS: single
     (D)   TOPOLOGY: linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCGGCATAT ACCAGGTGC   19

(2)   INFORMATION FOR SEQ ID NO: 43:

   (i)   SEQUENCE CHARACTERISTICS:
     (A)   LENGTH: 21 base pairs
     (B)   TYPE: nucleic acid
     (C)   STRANDEDNESS: single
     (D)   TOPOLOGY: linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATGGCTCA CTCGTAAATT C   21

(2)   INFORMATION FOR SEQ ID NO: 44:

   (i)   SEQUENCE CHARACTERISTICS:
     (A)   LENGTH: 21 base pairs
     (B)   TYPE: nucleic acid
     (C)   STRANDEDNESS: single
     (D)   TOPOLOGY: linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:44:

AACATTAGAC GCGTTAACGA G   21

(2)   INFORMATION FOR SEQ ID NO: 45:

   (i)   SEQUENCE CHARACTERISTICS:
     (A)   LENGTH: 21 base pairs
     (B)   TYPE: nucleic acid
     (C)   STRANDEDNESS: single
     (D)   TOPOLOGY: linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTCTTTTGAT GCCAGTCAGA G   21

(2)   INFORMATION FOR SEQ ID NO: 46:

   (i)   SEQUENCE CHARACTERISTICS:
     (A)   LENGTH: 22 base pairs
     (B)   TYPE: nucleic acid
     (C)   STRANDEDNESS: single
     (D)   TOPOLOGY: linear

   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCTACCCGG ATGGCTCTAA GG   22

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(2)   INFORMATION FOR SEQ ID NO: 47:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 25 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:47:

TATGGGAATT CGTGCCGTCC TGAAG   25

(2)   INFORMATION FOR SEQ ID NO: 48:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 21 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTGGGAGCA GTATACCAGC G   21

(2)   INFORMATION FOR SEQ ID NO: 49:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 21 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGCTATTGA GCAGGCTGCT C   21

(2)   INFORMATION FOR SEQ ID NO: 50:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 21 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCCATTAG TCTCTAAAAC C   21

(2)   INFORMATION FOR SEQ ID NO: 51:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 19 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:51:

GAGGTTTTCT GGAATCATC   19

(2)   INFORMATION FOR SEQ ID NO: 52:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 15 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCATAGGTGA GACTG                                          15
```

(2)   INFORMATION FOR SEQ ID NO: 53:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 18 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear


(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGTTACAGCC AGAAAACC                                       18
```

(2)   INFORMATION FOR SEQ ID NO: 54:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 33 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCATGGATCC TCGGCCTATT TTGCTGTTGC TCC                      33
```

(2)   INFORMATION FOR SEQ ID NO: 55:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 18 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGGCAGACCA CATATGTG                                       18
```

(2)   INFORMATION FOR SEQ ID NO: 56:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 20 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGTGCACTCC TGACCAAGCC                                     20
```

(2)   INFORMATION FOR SEQ ID NO: 57:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 19 base pairs
```

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```
                 (B)   TYPE:  nucleic acid
                 (C)   STRANDEDNESS: single
                 (D)   TOPOLOGY:  linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:57:

         ATTGGCTGCC ACTTTGTTC                              19


(2)   INFORMATION FOR SEQ ID NO: 58:

         (i)   SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 21 base pairs
                 (B)   TYPE:  nucleic acid
                 (C)   STRANDEDNESS: single
                 (D)   TOPOLOGY:  linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:58:

         ACCCTCATAC GTCACCACAA C                           21

(2)   INFORMATION FOR SEQ ID NO: 59:

         (i)   SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 24 base pairs
                 (B)   TYPE:  nucleic acid
                 (C)   STRANDEDNESS: single
                 (D)   TOPOLOGY:  linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:59:

         GCGGTGGACC ACATTAGGAT TATC                        24

(2)   INFORMATION FOR SEQ ID NO: 60:

         (i)   SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 19 base pairs
                 (B)   TYPE:  nucleic acid
                 (C)   STRANDEDNESS: single
                 (D)   TOPOLOGY:  linear

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:60:

         CATGATATGT CACCATCTG                              19


(2)   INFORMATION FOR SEQ ID NO: 61:

         (i)   SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 19 base pairs
                 (B)   TYPE:  nucleic acid
                 (C)   STRANDEDNESS: single
                 (D)   TOPOLOGY:  linear

         (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:61:

         GTCATCCATA ACGAGCTGG                              19

(2)   INFORMATION FOR SEQ ID NO: 62:

         (i)   SEQUENCE CHARACTERISTICS:
                 (A)   LENGTH: 33 base pairs
                 (B)   TYPE:  nucleic acid
```

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```
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCGGAATTC GAGGGGCGGC ATAAAGAACC AGG   33

(2)   INFORMATION FOR SEQ ID NO: 63:

```
    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 36 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGCTGAATT CGGATCACAA GCTCAGAGGC TATGCC   36

(2)   INFORMATION FOR SEQ ID NO: 64:

```
    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 30 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTATAACGGA TCCACATCTC CCCTTACCTC   30

(2)   INFORMATION FOR SEQ ID NO: 65:

```
    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 30 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:65:

TAACCTGGAT CCTTATGCCG CCCCTCTTAG   30

(2)   INFORMATION FOR SEQ ID NO: 66:

```
    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 38 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAATTGGATC CTGTGTCGGG TGGAATGAAT AACATGTC   38

(2)   INFORMATION FOR SEQ ID NO: 67:

```
    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 37 base pairs
        (B)   TYPE:  nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY:  linear
```

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATCGGCAGAT CTGATAGAGC GGGGACTTGC CGGATCC   37

(2)   INFORMATION FOR SEQ ID NO: 68:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 28 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:68:

TACCCTGCCC GCGCCCATAC TTTTGATG   28

(2)   INFORMATION FOR SEQ ID NO: 69:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 33 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGCTGAGATC TGGTTCGGGT CGCCAAGAAG GTG   33

(2)   INFORMATION FOR SEQ ID NO: 70:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 27 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:70:

TACAGATCTA TACAACTTAA CAGTCGG   27

(2)   INFORMATION FOR SEQ ID NO: 71:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 29 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCGGCAGATC TCACCGACAC CATTAGTAC   29

(2)   INFORMATION FOR SEQ ID NO: 72:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 28 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:72:

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CCGTCGGATC CCAGGGGCTG CTGTCCTG   28

(2)   INFORMATION FOR SEQ ID NO: 73:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 31 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAAGGAATTC AAGACCAGAG GTAGCCTCCT C   31

(2)   INFORMATION FOR SEQ ID NO: 74:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 28 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTTGATATGA ATTCAATAAC CTCGACGG   28

(2)   INFORMATION FOR SEQ ID NO: 75:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 36 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:75:

TTTGGATCCT CAGGGAGCGC GGAACGCAGA AATGAG   36

(2)   INFORMATION FOR SEQ ID NO: 76:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 26 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:76:

TCACTCGTGA ATTCCTATAC TAATAC   26

(2)   INFORMATION FOR SEQ ID NO: 77:

       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 34 base pairs
              (B)   TYPE: nucleic acid
              (C)   STRANDEDNESS: single
              (D)   TOPOLOGY: linear

       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTTGGATCCT CAGGGAGCGC GGAACGCAGA AATG   34

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(2)   INFORMATION FOR SEQ ID NO: 78:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 25 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:78:

TGATAGAGCG GGACTTGCCG GATCC   25

(2)   INFORMATION FOR SEQ ID NO: 79:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 24 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:79:

TTGCATTAGG TTAATGAGGA TCTC   24

(2)   INFORMATION FOR SEQ ID NO: 80:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 25 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACCTGCTTCC TTCAGCCTGC AGAAG   25

(2)   INFORMATION FOR SEQ ID NO: 81:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 29 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCGGTGGATC CGCTCCCAGG CGTCAAAAC   29

(2)   INFORMATION FOR SEQ ID NO: 82:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 29 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGGCGGATCG AATTCGAGAC CCTTCTTGG   29

(2)   INFORMATION FOR SEQ ID NO: 83:

```
(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 27 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:83:

AGGATGGATC CATAAGTTAC CGATCAG                              27


(2)   INFORMATION FOR SEQ ID NO: 84:

(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 29 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGCTGGAATT CCTCTGAGGA CGCCCTCAC                            29

(2)   INFORMATION FOR SEQ ID NO: 85:

(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 27 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCCGAAGATC TATCGGACAT AGACCTC                              27

(2)   INFORMATION FOR SEQ ID NO: 86:

(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 30 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGACGACGG ATCCCCTTGG ATATAGCCTG                           30

(2)   INFORMATION FOR SEQ ID NO: 87:

(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 40 base pairs
       (B)   TYPE:  nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY:  linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGCCGAATTC AGGCAGACCA CATATGTGGT CGATGCCATG                40

(2)   INFORMATION FOR SEQ ID NO: 88:

(i)    SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 25 base pairs
```

```
                   (B)   TYPE:  nucleic acid
                   (C)   STRANDEDNESS: single
                   (D)   TOPOLOGY:  linear

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:88:

          GCAGGTGTGC CTGGATCCGG CAAGT                                    25

(2)   INFORMATION FOR SEQ ID NO: 89:

          (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 30 base pairs
                   (B)   TYPE:  nucleic acid
                   (C)   STRANDEDNESS: single
                   (D)   TOPOLOGY:  linear

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:89:

          GTTAGAATTC CGGCCCAGCT GTGGTAGGTC                               30

(2)   INFORMATION FOR SEQ ID NO: 90:

          (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 24 base pairs
                   (B)   TYPE:  nucleic acid
                   (C)   STRANDEDNESS: single
                   (D)   TOPOLOGY:  linear

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:90:

          CCGTCCGATT GGTCTGTATG CAGG                                     24

(2)   INFORMATION FOR SEQ ID NO: 91:

          (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 22 base pairs
                   (B)   TYPE:  nucleic acid
                   (C)   STRANDEDNESS: single
                   (D)   TOPOLOGY:  linear

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:91:

          TACCAGTTTA CTGCAGGTGT GC                                       22

(2)   INFORMATION FOR SEQ ID NO: 92:

          (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 22 base pairs
                   (B)   TYPE:  nucleic acid
                   (C)   STRANDEDNESS: single
                   (D)   TOPOLOGY:  linear

          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:92:

          CAAGCCGATG TGGACGTTGT CG                                       22

(2)   INFORMATION FOR SEQ ID NO: 93:

          (i)   SEQUENCE CHARACTERISTICS:
                   (A)   LENGTH: 24 base pairs
                   (B)   TYPE:  nucleic acid
                   (C)   STRANDEDNESS: single
```

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```
            (D)    TOPOLOGY:  linear

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGCGCTGGGC CTGGTCACGC CAAG                                  24

(2)    INFORMATION FOR SEQ ID NO: 94:

    (i)    SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 22 base pairs
            (B)    TYPE:  nucleic acid
            (C)    STRANDEDNESS: single
            (D)    TOPOLOGY:  linear

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:94:

GCAGAAACTA GTGTTGACCC AG                                    22

(2)    INFORMATION FOR SEQ ID NO: 95:

    (i)    SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 22 base pairs
            (B)    TYPE:  nucleic acid
            (C)    STRANDEDNESS: single
            (D)    TOPOLOGY:  linear

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:95:

TAGGTCTACG ACGTGAGGCA AC                                    22

(2)    INFORMATION FOR SEQ ID NO: 96:

    (i)    SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 21 base pairs
            (B)    TYPE:  nucleic acid
            (C)    STRANDEDNESS: single
            (D)    TOPOLOGY:  linear

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:96:

TACAATCTTT CAGGAAGAAG G                                     21

(2)    INFORMATION FOR SEQ ID NO: 97:

    (i)    SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 21 base pairs
            (B)    TYPE:  nucleic acid
            (C)    STRANDEDNESS: single
            (D)    TOPOLOGY:  linear

    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCCACACTCC TCCATAATAG C                                     21

(2)    INFORMATION FOR SEQ ID NO: 98:

    (i)    SEQUENCE CHARACTERISTICS:
            (A)    LENGTH: 24 base pairs
            (B)    TYPE:  nucleic acid
            (C)    STRANDEDNESS: single
            (D)    TOPOLOGY:  linear
```

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(xi)   SEQUENCE DESCRIPTION: SEQ ID NO:98:

GATAGTGCTT TGCAGTGAGT ACCG   24

(2)   INFORMATION FOR SEQ ID NO: 99:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 30 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTATAACGGA TCCACATCTC CCCTTACCTC   30

(2)   INFORMATION FOR SEQ ID NO: 100:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 27 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:100:

TACAGATCTA TACAACTTAA CAGTCGG   27

(2)   INFORMATION FOR SEQ ID NO: 101:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 29 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCGGCAGATC TCACCGACAC CATTAGTAC   29

(2)   INFORMATION FOR SEQ ID NO: 102:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 30 base pairs
       (B)   TYPE: nucleic acid
       (C)   STRANDEDNESS: single
       (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:102:

TAACCTGGAT CCTTATGCCG CCCCTCTTAG   30

(2)   INFORMATION FOR SEQ ID NO: 103:

    (i)   SEQUENCE CHARACTERISTICS:
       (A)   LENGTH: 36 base pairs

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```
            (B)  TYPE:  nucleic acid
            (C)  STRANDEDNESS: single
            (D)  TOPOLOGY:  linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCACAACCTA GGTTACTATA ACTCCCGAGT TTTACC                        36


(2)  INFORMATION FOR SEQ ID NO: 104:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 33 base pairs
          (B)  TYPE:  nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY:  linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:104:

GGGTTCCCTA GGATGCGCCC TCGGCCTATT TTG                           33


(2)  INFORMATION FOR SEQ ID NO: 105:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 33 base pairs
          (B)  TYPE:  nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY:  linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGTGGGCCTA GGAGCGGCGG TTCCGGCGGT GGT                           33


(2)  INFORMATION FOR SEQ ID NO: 106:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 33 base pairs
          (B)  TYPE:  nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY:  linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCTTGGCCTA GGCAGGCCCA GCGCCCCGCC GCT                           33


(2)  INFORMATION FOR SEQ ID NO: 107:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 33 base pairs
          (B)  TYPE:  nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY:  linear

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCGCCACCTA GGGATGTTGA CTCCCGCGGC GCC                           33
```

(2)   INFORMATION FOR SEQ ID NO: 108:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 27 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTCGGATCCA TGGCGGTCGC TCCGGCC   27

(2)   INFORMATION FOR SEQ ID NO: 109:

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 33 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCAAGCTTAT CATCATAGCA CAGAGTGGGG GGC   33

(2)   INFORMATION FOR SEQ ID NO: 110

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 20 AMINO ACID RESIDUES
        (B)   TYPE: AMINO ACID
        (C)   STRANDNESS: UNKNOWN
        (D)   TOPOLOGY: UNKNOWN

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Ala Pro Leu Thr Ala Val Ala Pro Ala His Asp Thr Pro Pro
          5   10   15

Val Pro Asp Val Asp
         20

(2)   INFORMATION FOR SEQ ID NO: 111

    (i)   SEQUENCE CHARACTERISTICS:
        (A)   LENGTH: 20 AMINO ACID RESIDUES
        (B)   TYPE: AMINO ACID
        (C)   STRANDNESS: UNKNOWN
        (D)   TOPOLOGY: UNKNOWN

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ala Ala Pro Leu Thr Ala Val Ala Pro Ala His Asp Thr Pro Pro
          5   10   15

Val Pro Asp Val Asp
         20

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